

48

atg aca tcg ccc cag cta gag tgg act ctg cag acc ctt ctg gag cag	48
Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln	
1 5 10 15	
ctg aac gag gat gaa tta aag agt ttc aaa tcc ctt tta tgg gct ttt	96
Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe	
20 25 30	
ccc ctc gaa gac gtg cta cag aag acc cca tgg tct gag gtg gaa gag	144
Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu	
35 40 45	
gct gat ggc aag aaa ctg gca gaa att ctg gtc aac acc tcc tca gaa	192
Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu	
50 55 60	
aat tgg ata agg aat gcg act gtg aac atc ttg gaa gag atg aat ctc	240
Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu	
65 70 75 80	
acg gaa ttg tgt aag atg gca aag gct gag atg atg gag gac gga cag	288
Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln	
85 90 95	
gtg caa gaa ata gat aat cct gag ctg gga gat gca gaa gaa gac tcg	336
Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser	
100 105 110	
gag tta gca aag cca ggt gaa aag gaa gga tgg aga aat tca atg gag	384
Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu	
115 120 125	
aaa caa tct ttg gtc tgg aag aac acc ttt tgg caa gga gac att gac	432
Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp	
130 135 140	
aat ttc cat gac gac gtc act ctg aga aac caa cgg ttc att cca ttc	480
Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe	
145 150 155 160	
ttg aat ccc aga aca ccc agg aag cta aca cct tac acg gtg gtg ctg	528
Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu	
165 170 175	
cac ggc ccc gca ggc gtg ggg aaa acc acg ctg gcc aaa aag tgt atg	576
His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met	
180 185 190	
ctg gac tgg aca gac tgc aac ctc agc ccg acg ctc aga tac gcg ttc	624
Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe	
195 200 205	

FIG. 1A

672

tac ctc agc tgc aag gag ctc agc cgc atg ggc ccc tgc agt ttt gca	
Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala	
210 215 220	
gag ctg atc tcc aaa gac tgg cct gaa ttg cag gat gac att cca agc	720
Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser	
225 230 235 240	
atc cta gcc caa gca cag aga atc ctg ttc gtg gtc gat ggc ctt gat	768
Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp	
245 250 255	
gag ctg aaa gtc cca cct ggg gcg ctg atc cag gac atc tgc ggg gac	816
Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp	
260 265 270	
tgg gag aag aag aag ccg gtg ccc gtc ctc ctg ggg agt ttg ctg aag	864
Trp Glu Lys Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys	
275 280 285	
agg aag atg tta ccc agg gca gcc ttg ctg gtc acc acg cgg ccc agg	912
Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg	
290 295 300	
gca ctg agg gac ctc cag ctc ctg gcg cag cag ccg atc tac ata agg	960
Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Gln Pro Ile Tyr Ile Arg	
305 310 315 320	
gtg gag ggc ttc ctg gag gag gac agg agg gcc tat ttc ctg aga cac	1008
Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His	
325 330 335	
ttt gga gac gag gac caa gcc atg cgt gcc ttt gag cta atg agg agc	1056
Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser	
340 345 350	
aac gcg gcc ctg ttc cag ctg ggc tcg gcc ccc gcg gtg tgc tgg att	1104
Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile	
355 360 365	
gtg tgc acg act ctg aag ctg cag atg gag aag ggg gag gac ccg ccg	1152
Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro	
370 375 380	
gtt ccc gca ggg cgc aca gct gcg ggg cgc gct gcg gac gct gag cct	1200
Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro	
385 390 395 400	
cct ggc cgc gca ggg ctg tgg gcg cag atg tcc gtg ttc cac cga gag	1248
Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu	
405 410 415	

FIG. 1B

1296

gac ctg gaa agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc ctg
 Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu
 420 425 430

gac gga gac atc ctc cgc cag gac aga gtc tcc aaa ggc tgc tac tcc
 Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser
 435 440 445

ttc atc cac ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac gcc
 Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala
 450 455 460

ctg gag aag gag gag gag gag gac agg gac ggc cac gcc tgg gac att
 Leu Glu Lys Glu Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile
 465 470 475 480

ggg gac gta cag aag ctg ctt tcc gga gaa gaa aga ctc aag aac ccc
 Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro
 485 490 495

gac ctg att caa gta gga cac ttc tta ttc ggc ctc gct aac gag aag
 Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys
 500 505 510

aga gcc aag gag ttg gag gcc act ttt ggc tgc cgg atg tca ccg gac
 Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp
 515 520 525

atc aaa cag gaa ttg ctg caa tgc aaa gca cat ctt cat gca aat aag
 Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn Lys
 530 535 540

ccc tta tcc gtg acc gac ctg aag gag gtc ttg ggc tgc ctg tat gag
 Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr Glu
 545 550 555 560

tct cag gag gag gag ctg gcg aag gtg gtg gtg gcc ccg ttc aag gaa
 Ser Gln Glu Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys Glu
 565 570 575

att tct att cac ctg aca aat act tct gaa gtg atg cat tgt tcc ttc
 Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser Phe
 580 585 590

agc ctg aag cat tgt caa gac ttg cag aaa ctc tca ctg cag gta gca
 Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val Ala
 595 600 605

aag ggg gtg ttc ctg gag aat tac atg gat ttt gaa ctg gac att gaa
 Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile Glu
 610 615 620

1344

1392

1440

1488

1536

1584

1632

1680

1728

1776

1824

1872

FIG. 1C

ttt gaa agc tca aac agc aac ctc aag ttt ctg gaa gtg aaa caa agc
Phe Glu Ser Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser
625 630 635 640

ttc ctg agt gac tct tct gtg cgg att ctt tgt gac cac gta acc cgt
Phe Leu Ser Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg
645 650 655

agc acc tgt cat ctg cag aaa gtg gag att aaa aac gtc acc cct gac
Ser Thr Cys His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp
660 665 670

acc gcg tac cgg gac ttc tgt ctt gct ttc att ggg aag aag acc ctc
Thr Ala Tyr Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu
675 680 685

acg cac ctg acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg
Thr His Leu Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met
690 695 700

ctg atg ctg tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac
Leu Met Leu Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr
705 710 715 720

ctg agg ttg gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc
Leu Arg Leu Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe
725 730 735

ttc tat gtc ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca
Phe Tyr Val Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser
740 745 750

gcc aat gtg ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg
Ala Asn Val Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met
755 760 765

aca cgc cca aaa cac ttc ctg cag atg ttg tcg ttg gaa aac tgt cgt
Thr Arg Pro Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg
770 775 780

ctt aca gaa gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc
Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser
785 790 795 800

aag aag ctg aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca
Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr
805 810 815

ggg gtg aag ttt ctg t
Gly Val Lys Phe Leu
820

1920

1968

2016

2064

2112

2160

2208

2256

2304

2352

2400

2448

2464

FIG. 1D

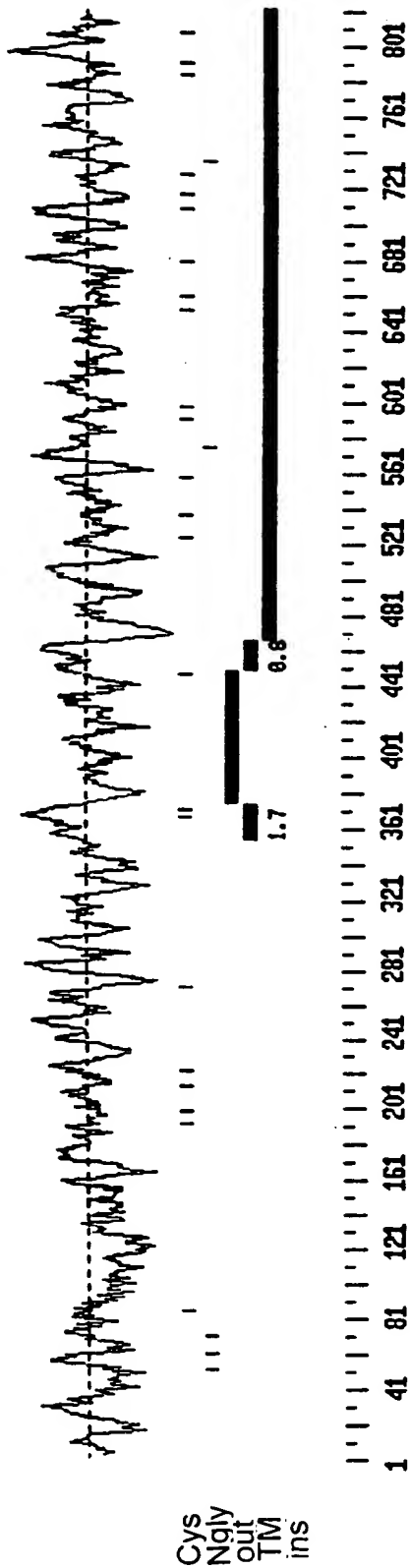


FIG. 2

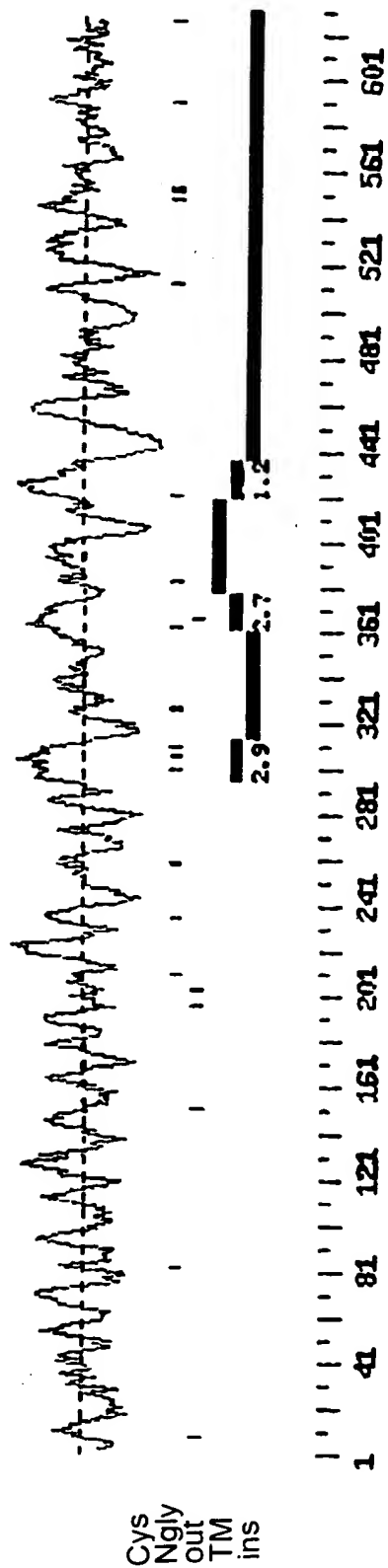
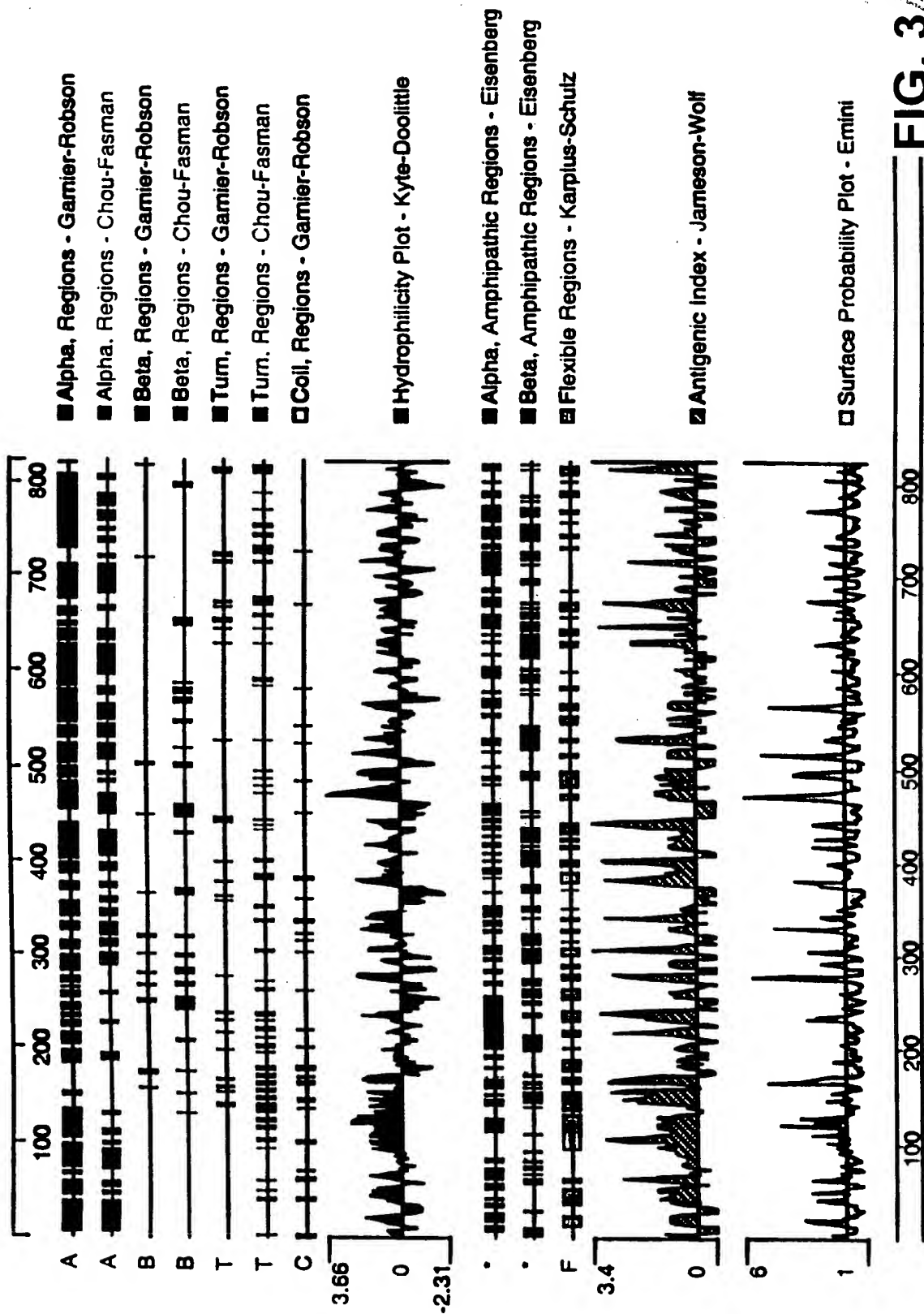


FIG. 6





NB-ARC: domain 1 of 1, from 176 to 190: score 11.4, E = 0.033
(SEQ ID NO: 9) *->ivGMGGiGKTTLakq<-*

NBS-2 176 190
++G++G+GKTTLak+
LHGPAGVGKTTLAKK

FIG. 4A

LRR_RI_2: domain 1 of 2, from 743 to 770: score 13.4, E = 0.57
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaealKs<-*
n+sL+ L+Ls N l deGa+ L ++ +
NBS-2 743 770
NQSLKHLRLSANVLLDEGAMLLYKTMTR

FIG. 4B

LRR_RI_2: domain 2 of 2, from 772 to 799: score 18.2, E = 0.12
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaealKs<-*
++ L+ L+L+n+ l+++ ++ La++L
NBS-2 772 799
KHFLQMLSENCRLTEASCKDLAAVLVV

FIG. 4C

LRR_RI_2: domain 1 of 1, from 596 to 623: score 11.0, E = 1.2
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaealKs<-*
++sLreL++ rN+l r L++sL++
NBS-3 596 623
NBSLRELHIFDNDLNGISERILSKALEH

FIG. 8



48

atg gca gaa tcg gat tct act gac ttt gac ctg ctg tgg tat cta gag	
Met Ala Glu Ser Asp Ser Thr Asp Phe Asp Leu Leu Trp Tyr Leu Glu	
1 5 10 15	
aat ctc agt gac aag gaa ttt cag agt ttt aag aag tat ctg gca cgc	96
Asn Leu Ser Asp Lys Glu Phe Gln Ser Phe Lys Lys Tyr Leu Ala Arg	
20 25 30	
aag att ctt gat ttc aaa ctg cca cag ttt cca ctg ata cag atg aca	144
Lys Ile Leu Asp Phe Lys Leu Pro Gln Phe Pro Leu Ile Gln Met Thr	
35 40 45	
aaa gaa gaa ctg gct aac gtg ttg cca atc tct tat gag gga cag tat	192
Lys Glu Glu Leu Ala Asn Val Leu Pro Ile Ser Tyr Glu Gly Gln Tyr	
50 55 60	
ata tgg aat atg ctc ttc agc ata ttt tca atg atg cgt aag gaa gat	240
Ile Trp Asn Met Leu Phe Ser Ile Phe Ser Met Met Arg Lys Glu Asp	
65 70 75 80	
ctt tgt agg aag atc att ggc aga cga aac cat gtg ttc tac ata ctt	288
Leu Cys Arg Lys Ile Ile Gly Arg Arg Asn His Val Phe Tyr Ile Leu	
85 90 95	
caa tta gcc tat gat tct acc agc tat tat tca gca aac aat ctc aat	336
Gln Leu Ala Tyr Asp Ser Thr Ser Tyr Tyr Ser Ala Asn Asn Leu Asn	
100 105 110	
gtg ttc ctg atg gga gag aga gca tct gga aaa act att gtt ata aat	384
Val Phe Leu Met Gly Glu Arg Ala Ser Gly Lys Thr Ile Val Ile Asn	
115 120 125	
ctg gct gtg ttg agg tgg atc aag ggt gag atg tgg cag aac atg atc	432
Leu Ala Val Leu Arg Trp Ile Lys Gly Glu Met Trp Gln Asn Met Ile	
130 135 140	
tcg tac gtc gtt cac ctc act gct cac gaa ata aac cag atg acc aac	480
Ser Tyr Val Val His Leu Thr Ala His Glu Ile Asn Gln Met Thr Asn	
145 150 155 160	
agc agc ttg gct gag cta atc gcc aag gac tgg cct gac ggc cag gct	528
Ser Ser Leu Ala Glu Leu Ile Ala Lys Asp Trp Pro Asp Gly Gln Ala	
165 170 175	
ccc att gca gac atc ctg tct gat ccc aag aaa ctc ctt ttc atc ctc	576
Pro Ile Ala Asp Ile Leu Ser Asp Pro Lys Lys Leu Leu Phe Ile Leu	
180 185 190	
gag gac ttg gac aac ata aga ttc gag tta aat gtc aat gaa agt gct	624
Glu Asp Leu Asp Asn Ile Arg Phe Glu Leu Asn Val Asn Glu Ser Ala	
195 200 205	

FIG. 5A

672

ttg tgt agt aac agc acc cag aaa gtt ccc att cca gtt ctc ctg gtc	
Leu Cys Ser Asn Ser Thr Gln Lys Val Pro Ile Pro Val Leu Leu Val	
210 215 220	
agt ttg ctg aag aga aaa atg gct cca ggc tgc tgg ttc ctc atc tcc	720
Ser Leu Leu Lys Arg Lys Met Ala Pro Gly Cys Trp Phe Leu Ile Ser	
225 230 235 240	
tca agg ccc aca cgt ggg aat aat gta aaa acg ttc ttg aaa gag gta	768
Ser Arg Pro Thr Arg Gly Asn Asn Val Lys Thr Phe Leu Lys Glu Val	
245 250 255	
gat tgc tgc acg acc ttg cag ctg tcg aat ggg aag agg gag ata tat	816
Asp Cys Cys Thr Thr Leu Gln Leu Ser Asn Gly Lys Arg Glu Ile Tyr	
260 265 270	
ttt aac tct ttc ttt aaa gac cgc cag agg gcg tcg gca gcc ctc cag	864
Phe Asn Ser Phe Phe Lys Asp Arg Gln Arg Ala Ser Ala Ala Leu Gln	
275 280 285	
ctt gta cat gag gat gaa ata ctc gtg ggt ctg tgc cga gtc gcc atc	912
Leu Val His Glu Asp Glu Ile Leu Val Gly Leu Cys Arg Val Ala Ile	
290 295 300	
tta tgc tgg atc acg tgt act gtc ctg aag cgg cag atg gac aag ggg	960
Leu Cys Trp Ile Thr Cys Thr Val Leu Lys Arg Gln Met Asp Lys Gly	
305 310 315 320	
cgt gac ttc cag ctc tgc tgc caa aca ccc act gat cta cat gcc cac	1008
Arg Asp Phe Gln Leu Cys Cys Gln Thr Pro Thr Asp Leu His Ala His	
325 330 335	
ttt ctt gct gat gcg ttg aca tca gag gct gga ctt act gcc aat cag	1056
Phe Leu Ala Asp Ala Leu Thr Ser Glu Ala Gly Leu Thr Ala Asn Gln	
340 345 350	
tat cac cta ggt ctc cta aaa cgt ctg tgt ttg ctg gct gca gga gga	1104
Tyr His Leu Gly Leu Leu Lys Arg Leu Cys Leu Leu Ala Ala Gly Gly	
355 360 365	
ctg ttt ctg agc acc ctg aat ttc agt ggt gaa gac ctc aga tgt gtt	1152
Leu Phe Leu Ser Thr Leu Asn Phe Ser Gly Glu Asp Leu Arg Cys Val	
370 375 380	
ggg ttt act gag gct gat gtc tct gtg ttg cag gcc gcg aat att ctt	1200
Gly Phe Thr Glu Ala Asp Val Ser Val Leu Gln Ala Ala Asn Ile Leu	
385 390 395 400	
ttg ccg agc aac act cat aaa gac cgt tac aag ttc ata cac ttg aac	1248
Leu Pro Ser Asn Thr His Lys Asp Arg Tyr Lys Phe Ile His Leu Asn	
405 410 415	

FIG. 5B

1296

gtc	cag	gag	ttt	tgt	aca	gcc	att	gca	ttt	ctg	atg	gca	gta	ccc	aac		
Val	Gln	Glu	Phe	Cys	Thr	Ala	Ile	Ala	Phe	Leu	Met	Ala	Val	Pro	Asn		
			420					425					430				
tat	ctg	atc	ccc	tca	ggc	agc	aga	gag	tat	aaa	gag	aag	aga	gaa	caa		1344
Tyr	Leu	Ile	Pro	Ser	Gly	Ser	Arg	Glu	Tyr	Lys	Glu	Lys	Arg	Glu	Gln		
		435					440					445					
tac	tct	gac	ttt	aat	caa	gtg	ttt	act	ttc	att	ttt	ggt	ctt	cta	aat		1392
Tyr	Ser	Asp	Phe	Asn	Gln	Val	Phe	Thr	Phe	Ile	Phe	Gly	Leu	Leu	Asn		
	450					455					460						
gca	aac	agg	aga	aag	att	ctt	gag	aca	tcc	ttt	gga	tac	cag	cta	ccg		1440
Ala	Asn	Arg	Arg	Lys	Ile	Leu	Glu	Thr	Ser	Phe	Gly	Tyr	Gln	Leu	Pro		
465					470				475					480			
atg	gta	gac	agc	ttc	aag	tgg	tac	tcg	gtg	gga	tac	atg	aaa	cat	ttg		1488
Met	Val	Asp	Ser	Phe	Lys	Trp	Tyr	Ser	Val	Gly	Tyr	Met	Lys	His	Leu		
			485					490					495				
gac	cgt	gac	ccg	gaa	aag	ttg	acg	cac	cat	atg	cct	ttg	ttt	tac	tgt		1536
Asp	Arg	Asp	Pro	Glu	Lys	Leu	Thr	His	His	Met	Pro	Leu	Phe	Tyr	Cys		
			500					505					510				
ctc	tat	gag	aat	cgg	gaa	gaa	gaa	ttt	gtg	aag	acg	att	gtg	gat	gct		1584
Leu	Tyr	Glu	Asn	Arg	Glu	Glu	Glu	Phe	Val	Lys	Thr	Ile	Val	Asp	Ala		
		515				520						525					
ctc	atg	gag	gtt	aca	gtt	tac	ctt	caa	tca	gac	aag	gat	atg	atg	gtc		1632
Leu	Met	Glu	Val	Thr	Val	Tyr	Leu	Gln	Ser	Asp	Lys	Asp	Met	Met	Val		
	530					535					540						
tca	tta	tac	tgt	ctg	gat	tac	tgc	tgt	cac	ctg	agg	aca	ctt	aag	ttg		1680
Ser	Leu	Tyr	Cys	Leu	Asp	Tyr	Cys	Cys	His	Leu	Arg	Thr	Leu	Lys	Leu		
545				550				555						560			
agt	gtt	cag	cgc	atc	ttt	caa	aac	aaa	gag	cca	ctt	ata	agg	cca	act		1728
Ser	Val	Gln	Arg	Ile	Phe	Gln	Asn	Lys	Glu	Pro	Leu	Ile	Arg	Pro	Thr		
			565					570					575				
gct	agt	caa	atg	aag	agc	ctt	gtc	tac	tgg	aga	gag	atc	tgc	tct	ctt		1776
Ala	Ser	Gln	Met	Lys	Ser	Leu	Val	Tyr	Trp	Arg	Glu	Ile	Cys	Ser	Leu		
		580					585					590					
ttt	tat	aca	atg	gag	agc	ctc	cgg	gag	ctg	cat	atc	ttt	gac	aat	gac		1824
Phe	Tyr	Thr	Met	Glu	Ser	Leu	Arg	Glu	Leu	His	Ile	Phe	Asp	Asn	Asp		
		595				600					605						
ctt	aat	ggt	att	tca	gaa	agg	att	ctg	tct	aaa	gcc	ctg	gag	cat	tct		1872
Leu	Asn	Gly	Ile	Ser	Glu	Arg	Ile	Leu	Ser	Lys	Ala	Leu	Glu	His	Ser		
	610					615					620						

FIG. 5C



agc tgt aaa ctt cgc aca ctc aa
Ser Cys Lys Leu Arg Thr Leu
625 630

1895

FIG. 5D

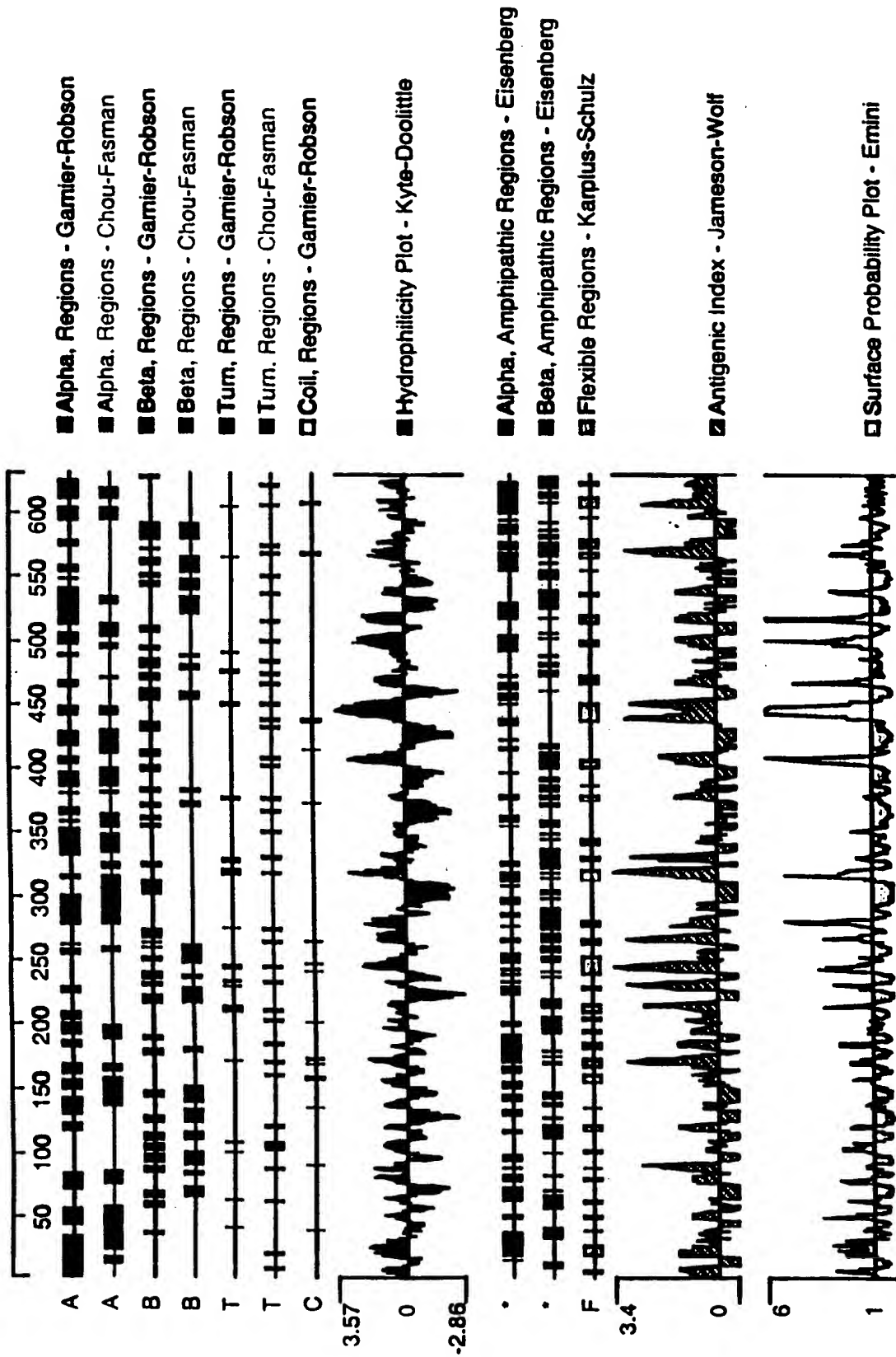


FIG. 7

100 150 200 250 300 350 400 450 500 550 600

48

atg aag gct gaa cta ctg gag aca tgg gac aac atc agt tgg cct aaa	
Met Lys Ala Glu Leu Leu Glu Thr Trp Asp Asn Ile Ser Trp Pro Lys	
1 5 10 15	
gac cac gta tat atc cgt aat aca tca aag gac gaa cat gag gaa ctg	96
Asp His Val Tyr Ile Arg Asn Thr Ser Lys Asp Glu His Glu Glu Leu	
20 25 30	
cag cgc cta ctg gat cct aat agg act aga gcc cag gcc cag acg ata	144
Gln Arg Leu Leu Asp Pro Asn Arg Thr Arg Ala Gln Ala Gln Thr Ile	
35 40 45	
gtc ttg gtg ggg agg gca ggg gtt ggg aag acc acc ttg gca atg cag	192
Val Leu Val Gly Arg Ala Gly Val Gly Lys Thr Thr Leu Ala Met Gln	
50 55 60	
gct atg ctg cac tgg gca aat gga gtt ctc ttt cag caa agg ttc tcc	240
Ala Met Leu His Trp Ala Asn Gly Val Leu Phe Gln Gln Arg Phe Ser	
65 70 75 80	
tat gtt ttc tat ctc agc tgc cat aaa ata agg tac atg aag gaa act	288
Tyr Val Phe Tyr Leu Ser Cys His Lys Ile Arg Tyr Met Lys Glu Thr	
85 90 95	
acc ttt gct gaa ttg att tct ttg gat tgg ccc gat ttt gat gcc ccc	336
Thr Phe Ala Glu Leu Ile Ser Leu Asp Trp Pro Asp Phe Asp Ala Pro	
100 105 110	
att gaa gag ttc atg tct caa cca gag aag ctc ctg ttt att att gat	384
Ile Glu Glu Phe Met Ser Gln Pro Glu Lys Leu Leu Phe Ile Ile Asp	
115 120 125	
ggc ttt gag gaa ata atc ata tct gag tca cgc tct gag agc ttg gat	432
Gly Phe Glu Glu Ile Ile Ile Ser Glu Ser Arg Ser Glu Ser Leu Asp	
130 135 140	
gat ggc tgc cca tgt aca gac tgg tac cag gag ctc cca gtg acc aaa	480
Asp Gly Ser Pro Cys Thr Asp Trp Tyr Gln Glu Leu Pro Val Thr Lys	
145 150 155 160	
atc cta cac agc ttg ttg aag aaa gaa ttg gtt ccc ctg gct acc tta	528
Ile Leu His Ser Leu Leu Lys Lys Glu Leu Val Pro Leu Ala Thr Leu	
165 170 175	
ctg atc acg atc aag acc tgg ttt gtg aga gat ctt aag gcc tca tta	576
Leu Ile Thr Ile Lys Thr Trp Phe Val Arg Asp Leu Lys Ala Ser Leu	
180 185 190	
gtg aat cca tgc ttt gta caa att aca ggg ttc aca ggg gac gac cta	624
Val Asn Pro Cys Phe Val Gln Ile Thr Gly Phe Thr Gly Asp Asp Leu	
195 200 205	

FIG. 9A

672

cgg gta tat ttc atg aga cac ttt gat gac tca agt gaa gtt gag aaa	
Arg Val Tyr Phe Met Arg His Phe Asp Asp Ser Ser Glu Val Glu Lys	
210 215 220	
atc ctg cag cag cta aga aaa aac gaa act ctc ttt cat tcc tgc agt	720
Ile Leu Gln Gln Leu Arg Lys Asn Glu Thr Leu Phe His Ser Cys Ser	
225 230 235 240	
gcc ccc atg gtg tgt tgg acc gta tgt tcc tgt ctg aag cag ccg aag	768
Ala Pro Met Val Cys Trp Thr Val Cys Ser Cys Leu Lys Gln Pro Lys	
245 250 255	
gtg agg tat tac gat ctc cag tca atc act cag act acc acc agt ctg	816
Val Arg Tyr Tyr Asp Leu Gln Ser Ile Thr Gln Thr Thr Thr Ser Leu	
260 265 270	
tat gcc tat ttt ttc tcc aac ttg ttc tcc aca gca gag gta gat ttg	864
Tyr Ala Tyr Phe Phe Ser Asn Leu Phe Ser Thr Ala Glu Val Asp Leu	
275 280 285	
gca gat gac agc tgg cca gga caa tgg agg gcc ctc tgc agt ctg gcc	912
Ala Asp Asp Ser Trp Pro Gly Gln Trp Arg Ala Leu Cys Ser Leu Ala	
290 295 300	
ata gaa ggg ctg tgg tct atg aac ttc acg ttt aac aaa gaa gac act	960
Ile Glu Gly Leu Trp Ser Met Asn Phe Thr Phe Asn Lys Glu Asp Thr	
305 310 315 320	
gag atc gag ggc ctg gaa gtg cct ttc att gat tct ctc tac gag ttc	1008
Glu Ile Glu Gly Leu Glu Val Pro Phe Ile Asp Ser Leu Tyr Glu Phe	
325 330 335	
aat att ctt caa aag atc aat gac tgt ggg ggt tgc act act ttc acc	1056
Asn Ile Leu Gln Lys Ile Asn Asp Cys Gly Gly Cys Thr Thr Phe Thr	
340 345 350	
cac cta agt ttc cag gag ttt ttt gca gcc atg tcc ttt gtg cta gag	1104
His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Ser Phe Val Leu Glu	
355 360 365	
gaa cct aga gaa ttc cct ccc cat tcc aca aag cca caa gag atg aag	1152
Glu Pro Arg Glu Phe Pro Pro His Ser Thr Lys Pro Gln Glu Met Lys	
370 375 380	
atg tta ctg caa cac gtc ttg ctt gac aaa gaa gcc tac tgg act cca	1200
Met Leu Leu Gln His Val Leu Leu Asp Lys Glu Ala Tyr Trp Thr Pro	
385 390 395 400	
gtg gtt ctg ttc ttc ttt ggt ctt tta aat aaa aac ata gca aga gaa	1248
Val Val Leu Phe Phe Phe Gly Leu Leu Asn Lys Asn Ile Ala Arg Glu	
405 410 415	

FIG. 9B

ctg gaa gat act ttg cat tgt aaa ata tct ccc agg gta atg gag gaa 1296
 Leu Glu Asp Thr Leu His Cys Lys Ile Ser Pro Arg Val Met Glu Glu
 420 425 430

tta tta aag tgg gga gaa gag tta ggt aag gct gaa agt gcc tct ctc 1344
 Leu Leu Lys Trp Gly Glu Glu Leu Gly Lys Ala Glu Ser Ala Ser Leu
 435 440 445

caa ttt cac att cta cga ctt ttt cac tgc cta cac gag tcc cag gag 1392
 Gln Phe His Ile Leu Arg Leu Phe His Cys Leu His Glu Ser Gln Glu
 450 455 460

gaa gac ttc aca aag aag atg ttg ggt cgt atc ttt gaa gtt gac ctt 1440
 Glu Asp Phe Thr Lys Lys Met Leu Gly Arg Ile Phe Glu Val Asp Leu
 465 470 475 480

aat att ttg gag gac gaa gaa ctc caa gct tct tca ttt tgc cta aag 1488
 Asn Ile Leu Glu Asp Glu Glu Leu Gln Ala Ser Ser Phe Cys Leu Lys
 485 490 495

cac tgt aaa agg tta aat aag cta agg ctt tct gtt agc agt cac atc 1536
 His Cys Lys Arg Leu Asn Lys Leu Arg Leu Ser Val Ser Ser His Ile
 500 505 510

ctt gaa agg gac ttg gaa att ctg gag tga 1566
 Leu Glu Arg Asp Leu Glu Ile Leu Glu
 515 520

FIG. 9C

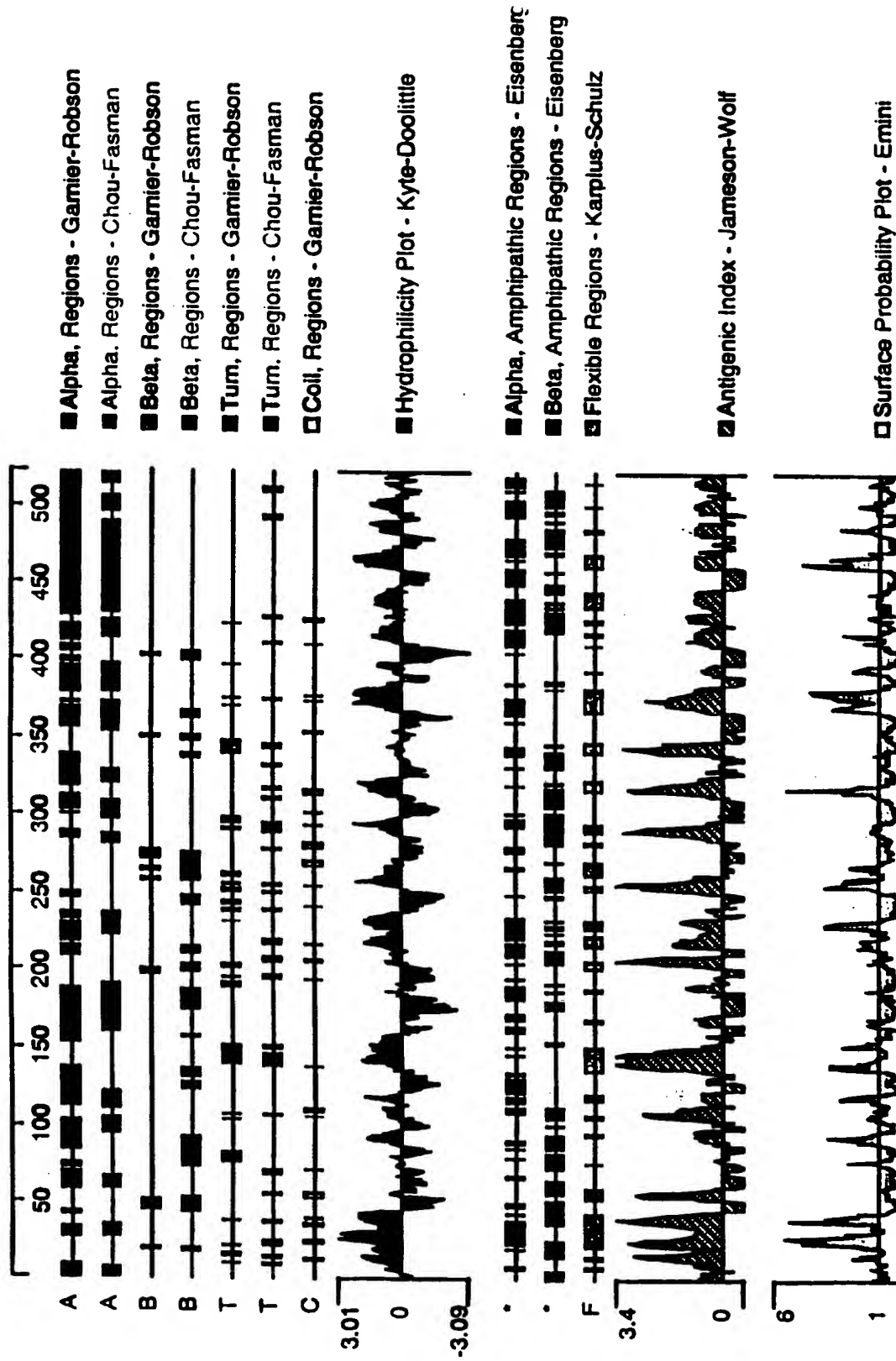


FIG. 11

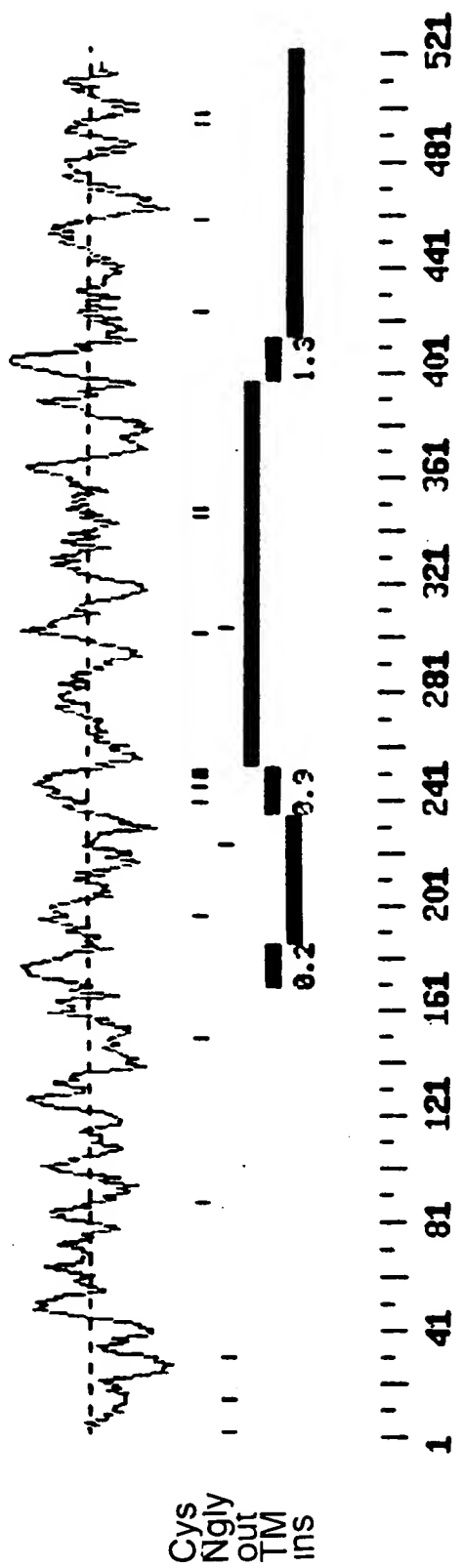


FIG. 10

NB-ARC: domain 1 of 1, from 50 to 79: score 9.4, E = 0.12
(SEQ ID NO:11) *->ivGMGGiGKTTLaqiyndes..gevqrhP<-*
+VG++G+GKTTLa q+ ++++ ++q +F
NBS-4 50 LVGRAGVGKTTLAMQAMLHWangVLFQQR 79

FIG. 12



c agc cgc tta tgg tcc agc aag tct gtc act gag att cac cta tac ttt 149
Ser Arg Leu Trp Ser Ser Lys Ser Val Thr Glu Ile His Leu Tyr Phe
1 5 10 15

gag gag gaa gtc aag caa gaa gaa tgt gac cat ttg gac cgc ctt ttt 97
Glu Glu Glu Val Lys Gln Glu Glu Cys Asp His Leu Asp Arg Leu Phe
20 25 30

gct ccc aag gaa gct ggg aaa cag cca cgt aca gtg atc att caa gga 145
Ala Pro Lys Glu Ala Gly Lys Gln Pro Arg Thr Val Ile Ile Gln Gly
35 40 45

cca caa gga att gga aaa acg aca ctc ctg atg aag ctg atg atg gcc 193
Pro Gln Gly Ile Gly Lys Thr Thr Leu Leu Met Lys Leu Met Met Ala
50 55 60

tgg tgc gac aac aag atc ttt cgg gat agg ttc ctg tac acg ttc tat 241
Trp Ser Asp Asn Lys Ile Phe Arg Asp Arg Phe Leu Tyr Thr Phe Tyr
65 70 75 80

ttc tgc tgc aga gaa ctg agg gag ttg ccg cca acg agt ttg gct gac 289
Phe Cys Cys Arg Glu Leu Arg Glu Leu Pro Pro Thr Ser Leu Ala Asp
85 90 95

ttg att tcc aga gag tgg cct gac ccc gct gct cct ata aca gag atc 337
Leu Ile Ser Arg Glu Trp Pro Asp Pro Ala Ala Pro Ile Thr Glu Ile
100 105 110

gtg tct caa ccg gag aga ctc ttg ttc gtc atc gac agc ttc gaa gag 385
Val Ser Gln Pro Glu Arg Leu Leu Phe Val Ile Asp Ser Phe Glu Glu
115 120 125

ctg cag ggc ggc ttg aac gaa ccc gat tgc gat ctg tgt ggt gac ttg 433
Leu Gln Gly Gly Leu Asn Glu Pro Asp Ser Asp Leu Cys Gly Asp Leu
130 135 140

atg gag aaa cgg ccg gtg cag gtg ctt ctg agc agt ttg ctg agg aag 481
Met Glu Lys Arg Pro Val Gln Val Leu Leu Ser Ser Leu Leu Arg Lys
145 150 155 160

aag atg ctc ccg gag gcc tcc ctg ctc atc gct atc aaa ccc gtg tgc 529
Lys Met Leu Pro Glu Ala Ser Leu Leu Ile Ala Ile Lys Pro Val Cys
165 170 175

ccg aag gag ctc cgg gat cag gtg acg atc tca gaa atc tac cag ccc 577
Pro Lys Glu Leu Arg Asp Gln Val Thr Ile Ser Glu Ile Tyr Gln Pro
180 185 190

cgg gga ttc aac gag agt gat agg tta gtg tat ttc tgc tgt ttc ttc 625
Arg Gly Phe Asn Glu Ser Asp Arg Leu Val Tyr Phe Cys Cys Phe Phe
195 200 205

FIG. 13A

673

aaa gac ccg aaa aga gcc atg gaa gcc ttc aat ctt gta aga gaa agt	
Lys Asp Pro Lys Arg Ala Met Glu Ala Phe Asn Leu Val Arg Glu Ser	
210 215 220	
gaa cag ctg ttt tcc ata tgc caa atc ccg ctc ctc tgc tgg atc ctg	721
Glu Gln Leu Phe Ser Ile Cys Gln Ile Pro Leu Leu Cys Trp Ile Leu	
225 230 235 240	
tgt acc agt ctg aag caa gag atg cag aaa gga aaa gac ctg gcc ctg	769
Cys Thr Ser Leu Lys Gln Glu Met Gln Lys Gly Lys Asp Leu Ala Leu	
245 250 255	
acc tgc cag agc act acc tct gtg tac tcc tct ttc gtc ttt aac ctg	817
Thr Cys Gln Ser Thr Thr Ser Val Tyr Ser Ser Phe Val Phe Asn Leu	
260 265 270	
ttc aca cct gag ggt gcc gag ggc ccg act ccg caa acc cag cac cag	865
Phe Thr Pro Glu Gly Ala Glu Gly Pro Thr Pro Gln Thr Gln His Gln	
275 280 285	
ctg aag gcc ctg tgc tcc ctg gct gca gag ggt atg tgg aca gac aca	913
Leu Lys Ala Leu Cys Ser Leu Ala Ala Glu Gly Met Trp Thr Asp Thr	
290 295 300	
ttt gag ttt tgt gaa gac gac ctc cgg aga aat ggg gtt gtt gac gct	961
Phe Glu Phe Cys Glu Asp Asp Leu Arg Arg Asn Gly Val Val Asp Ala	
305 310 315 320	
gac atc cct gcg ctg ctg ggc acc aag ata ctt ctg aag tac ggg gag	1009
Asp Ile Pro Ala Leu Leu Gly Thr Lys Ile Leu Leu Lys Tyr Gly Glu	
325 330 335	
cgt gag agc tcc tac gtg ttc ctc cac gtg tgt atc cag gag ttc tgt	1057
Arg Glu Ser Ser Tyr Val Phe Leu His Val Cys Ile Gln Glu Phe Cys	
340 345 350	
gcc gcc ttg ttc tat ttg ctc aag agc cac ctt gat cat cct cac cca	1105
Ala Ala Leu Phe Tyr Leu Leu Lys Ser His Leu Asp His Pro His Pro	
355 360 365	
gct gtg aga tgt gta cag gaa ttg cta gtt gcc aat ttt gaa aaa gca	1153
Ala Val Arg Cys Val Gln Glu Leu Leu Val Ala Asn Phe Glu Lys Ala	
370 375 380	
agg aga gca cat tgg att ttt ttg ggg tgt ttt cta act ggc ctt tta	1201
Arg Arg Ala His Trp Ile Phe Leu Gly Cys Phe Leu Thr Gly Leu Leu	
385 390 395 400	
aat aaa aag gaa caa gaa aaa ctg gat gcg ttt ttt ggc ttc caa ctg	1249
Asn Lys Lys Glu Gln Glu Lys Leu Asp Ala Phe Phe Gly Phe Gln Leu	
405 410 415	

FIG. 13B

tcc caa gag ata aag cag caa att cac cag tgc ctg aag agc tta ggg
Ser Gln Glu Ile Lys Gln Gln Ile His Gln Cys Leu Lys Ser Leu Gly
420 425 430



gag cgt ggc aat cct cag gga cag gtg gat tcc ttg gcg ata ttt tac
Glu Arg Gly Asn Pro Gln Gly Gln Val Asp Ser Leu Ala Ile Phe Tyr
435 440 445 1345

tgt ctc ttt gaa atg cag gat cct gcc ttt gtg aag cag gca gtg aac
Cys Leu Phe Glu Met Gln Asp Pro Ala Phe Val Lys Gln Ala Val Asn
450 455 460 1393

ctc ctc caa gaa gct aac ttt cat att att gac aac gtg gac ttg gtg
Leu Leu Gln Glu Ala Asn Phe His Ile Ile Asp Asn Val Asp Leu Val
465 470 475 480 1441

gtt tct gcc tac tgc tta aaa tac tgc tcc agc ttg agg aaa ctc tgt
Val Ser Ala Tyr Cys Leu Lys Tyr Cys Ser Ser Leu Arg Lys Leu Cys
485 490 495 1489

ttt tcc gtt caa aat gtc ttt aag aaa gag gat gaa cac agc tct acg
Phe Ser Val Gln Asn Val Phe Lys Lys Glu Asp Glu His Ser Ser Thr
500 505 510 1537

tcg gat tac agc ctc atc tgt tgg cat cac atc tgc tct gtg ctc acc
Ser Asp Tyr Ser Leu Ile Cys Trp His His Ile Cys Ser Val Leu Thr
515 520 525 1585

acc agc ggg cac ctc aga gag ctc cag gtg cag gac agc acc ctc agc
Thr Ser Gly His Leu Arg Glu Leu Gln Val Gln Asp Ser Thr Leu Ser
530 535 540 1633

gag tcg acc ttt gtg acc tgg tgt aac cag ctg agg cat ccc agc tgt
Glu Ser Thr Phe Val Thr Trp Cys Asn Gln Leu Arg His Pro Ser Cys
545 550 555 560 1681

cgc ctt cag aag ctt gga ata aat aac gtt tcc ttt tct ggc cag agt
Arg Leu Gln Lys Leu Gly Ile Asn Asn Val Ser Phe Ser Gly Gln Ser
565 570 575 1729

gtt ctg ctc ttt gag gtg ctc ttt tat cag cca gac ttg aaa tac ctg
Val Leu Leu Phe Glu Val Leu Phe Tyr Gln Pro Asp Leu Lys Tyr Leu
580 585 590 1777

agc ttc acc ctc acg aaa ctc tct cgt gat gac atc agg tcc ctc tgt
Ser Phe Thr Leu Thr Lys Leu Ser Arg Asp Asp Ile Arg Ser Leu Cys
595 600 605 1825

gat gcc ttg aac tac cca gca ggc aac gtc aaa gag cta gcg ctg gta
Asp Ala Leu Asn Tyr Pro Ala Gly Asn Val Lys Glu Leu Ala Leu Val
610 615 620 1873

FIG. 13C

gta ctc tgt gag gcc ctg aga cac cca gag tgt gcc ctg cag gtg ctc 2545
Val Leu Cys Glu Ala Leu Arg His Pro Glu Cys Ala Leu Gln Val Leu
835 840 845

ggg gtt gtt gca gga gta aga acc aag cag 2575
Gly Val Val Ala Gly Val Arg Thr Lys Gln
850 855

FIG. 13E

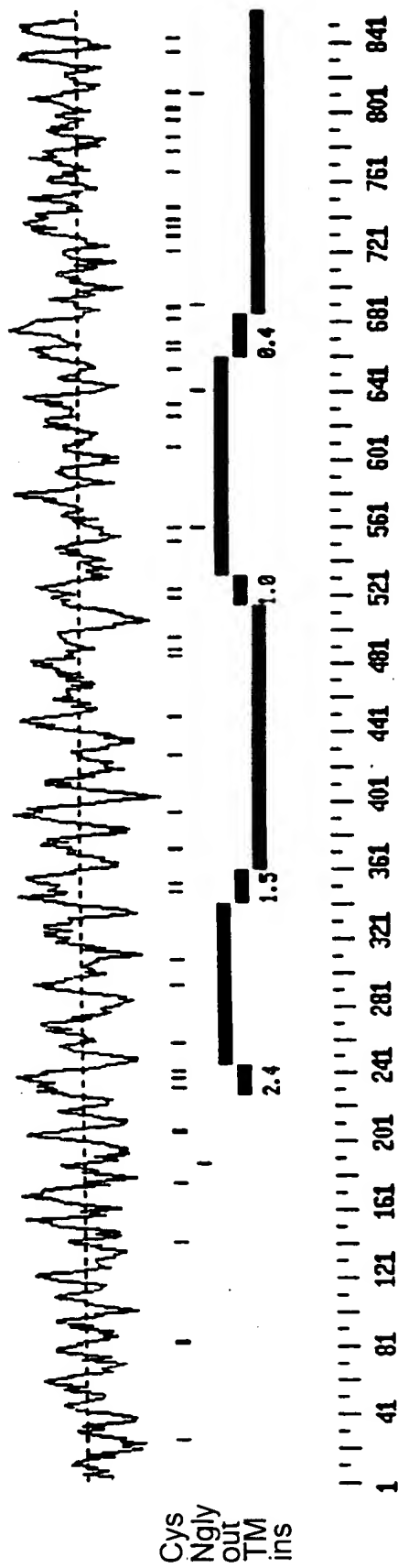


FIG. 14



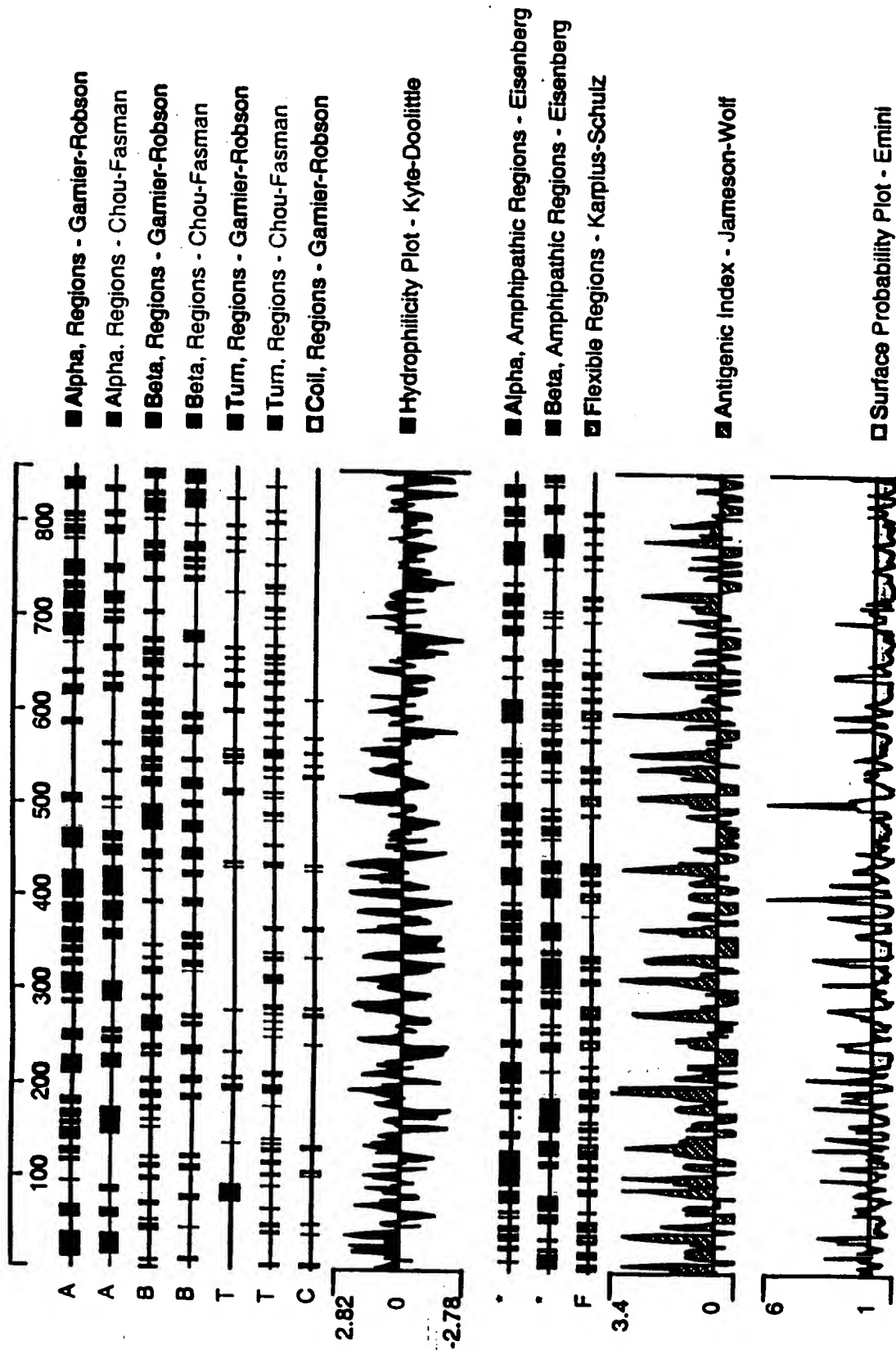


FIG. 15

100 200 300 400 500 600 700 800



LRR_RI_2: domain 1 of 8, from 530 to 557: score 6.4, E = 5.6
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaeaLks<-*

NBS-5 530 SGHLRELQVQDSTLSESTFVTWCNQLRH 557

FIG. 16A

LRR_RI_2: domain 2 of 8, from 615 to 642: score 5.2, E = 8.4
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaeaLks<-*

NBS-5 615 AGNVKELALVNCHLSPIDCEVLGGLTN 642

FIG. 16B

LRR_RI_2: domain 3 of 8, from 643 to 669: score 9.3, E = 2.2
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaeaLks<-*

NBS-5 643 NKKLTYLNVSCNQL-DTGVPLLCEALCS 669

FIG. 16C

LRR_RI_2: domain 4 of 8, from 699 to 726: score 32.8, E = 7.9e-06
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaeaLks<-*

NBS-5 699 NKSVMRYLDLSANVLKDEGLKTLCEALKH 726

FIG. 16D

LRR_RI_2: domain 5 of 8, from 728 to 755: score 10.0, E = 1.8
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaeaLks<-*

NBS-5 728 DCCLDSLCLVKCFITAAGCEDLASALIS 755

FIG. 16E

LRR_RI_2: domain 6 of 8, from 756 to 783: score 30.9, E = 3e-05
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaeaLks<-*

NBS-5 756 NQNLKILOIGCNEIGDVGVLQLLCRALTH 783

FIG. 16F

LRR_RI_2: domain 7 of 8, from 785 to 812: score 8.0, E = 3.3
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaeaLks<-*

NBS-5 785 DCRLEILGLEECGLTSTCKDLASVLTC 812

FIG. 16G

LRR_RI_2: domain 8 of 8, from 813 to 840: score 17.6, E = 0.14
(SEQ ID NO:10) *->npsLreLdLsnNklgdeGaraLaeaLks<-*

NBS-5 813 SKFLQQLNLTNTLDHTGVVVLCEALRH 840

FIG. 16H



gaattcgaat tctggggaagt tcttcagcct taacctaaagg tctcatactc ggagcact	
atg aca tcg ccc cag cta gag tgg act ctg cag acc ctt ctg gag cag	
Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln	
1 5 10 15	
ctg aac gag gat gaa tta aag agt ttc aaa tcc ctt tta tgg gct ttt	154
Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe	
20 25 30	
ccc ctc gaa gac gtg cta cag aag acc cca tgg tct gag gtg gaa gag	202
Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu	
35 40 45	
gct gat ggc aag aaa ctg gca gaa att ctg gtc aac acc tcc tca gaa	250
Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu	
50 55 60	
aat tgg ata agg aat gcg act gtg aac atc ttg gaa gag atg aat ctc	298
Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu	
65 70 75 80	
acg gaa ttg tgt aag atg gca aag gct gag atg atg gag gac gga cag	346
Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln	
85 90 95	
gtg caa gaa ata gat aat cct gag ctg gga gat gca gaa gaa gac tcg	394
Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser	
100 105 110	
gag tta gca aag cca ggt gaa aag gaa gga tgg aga aat tca atg gag	442
Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu	
115 120 125	
aaa cag tct ttg gtc tgg aag aac acc ttt tgg caa gga gac att gac	490
Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp	
130 135 140	
aat ttc cat gac gac gtc act ctg aga aac caa cgg ttc att cca ttc	538
Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe	
145 150 155 160	
ttg aat ccc aga aca ccc agg aag cta aca cct tac acg gtg gtg ctg	586
Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu	
165 170 175	
cac ggc ccc gca ggc gtg ggg aaa acc acg ctg gcc aaa aag tgt atg	634
His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met	
180 185 190	
ctg gac tgg aca gac tgc aac ctc agc ccg acg ctc aga tac gcg ttc	682
Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe	
195 200 205	
tac ctc agc tgc aag gag ctc agc cgc atg ggc ccc tgc agt ttt gca	730
Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala	
210 215 220	

FIG. 17A

778

gag	ctg	atc	tcc	aaa	gac	tgg	cct	gaa	ttg	cag	gat	gac	att	cca	agc	
Glu	Leu	Ile	Ser	Lys	Asp	Trp	Pro	Glu	Leu	Gln	Asp	Asp	Ile	Pro	Ser	
225					230					235					240	
atc	cta	gcc	caa	gca	cag	aga	atc	ctg	ttc	gtg	gtc	gat	ggc	ctt	gat	826
Ile	Leu	Ala	Gln	Ala	Gln	Arg	Ile	Leu	Phe	Val	Val	Asp	Gly	Leu	Asp	
				245					250					255		
gag	ctg	aaa	gtc	cca	cct	ggg	gcg	ctg	atc	cag	gac	atc	tgc	ggg	gac	874
Glu	Leu	Lys	Val	Pro	Pro	Gly	Ala	Leu	Ile	Gln	Asp	Ile	Cys	Gly	Asp	
			260					265					270			
tgg	gag	aag	aag	aag	ccg	gtg	ccc	gtc	ctc	ctg	ggg	agt	ttg	ctg	aag	922
Trp	Glu	Lys	Lys	Lys	Pro	Val	Pro	Val	Leu	Leu	Gly	Ser	Leu	Leu	Lys	
		275					280					285				
agg	aag	atg	tta	ccc	agg	gca	gcc	ttg	ctg	gtc	acc	acg	cgg	ccc	agg	970
Arg	Lys	Met	Leu	Pro	Arg	Ala	Ala	Leu	Leu	Val	Thr	Thr	Arg	Pro	Arg	
	290					295					300					
gca	ctg	agg	gac	ctc	cag	ctc	ctg	gcg	cag	cag	ccg	atc	tac	gta	agg	1018
Ala	Leu	Arg	Asp	Leu	Gln	Leu	Leu	Ala	Gln	Gln	Pro	Ile	Tyr	Val	Arg	
305					310					315					320	
gtg	gag	ggc	ttc	ctg	gag	gag	gac	agg	agg	gcc	tat	ttc	ctg	aga	cac	1066
Val	Glu	Gly	Phe	Leu	Glu	Glu	Asp	Arg	Arg	Ala	Tyr	Phe	Leu	Arg	His	
				325					330					335		
ttt	gga	gac	gag	gac	caa	gcc	atg	cgt	gcc	ttt	gag	cta	atg	agg	agc	1114
Phe	Gly	Asp	Glu	Asp	Gln	Ala	Met	Arg	Ala	Phe	Glu	Leu	Met	Arg	Ser	
			340					345					350			
aac	gcg	gcc	ctg	ttc	cag	ctg	ggc	tcg	gcc	ccc	gcg	gtg	tgc	tgg	att	1162
Asn	Ala	Ala	Leu	Phe	Gln	Leu	Gly	Ser	Ala	Pro	Ala	Val	Cys	Trp	Ile	
		355					360					365				
gtg	tgc	acg	act	ctg	aag	ctg	cag	atg	gag	aag	ggg	gag	gac	ccg	gtc	1210
Val	Cys	Thr	Thr	Leu	Lys	Leu	Gln	Met	Glu	Lys	Gly	Glu	Asp	Pro	Val	
	370					375					380					
ccc	acc	tgc	ctc	acc	cgc	acg	ggg	ctg	ttc	ctg	cgt	ttc	ctc	tgc	agc	1258
Pro	Thr	Cys	Leu	Thr	Arg	Thr	Gly	Leu	Phe	Leu	Arg	Phe	Leu	Cys	Ser	
385					390					395					400	
cgg	ttc	ccg	cag	ggc	gca	cag	ctg	cgg	ggc	gcg	ctg	cgg	acg	ctg	agc	1306
Arg	Phe	Pro	Gln	Gly	Ala	Gln	Leu	Arg	Gly	Ala	Leu	Arg	Thr	Leu	Ser	
				405					410					415		
ctc	ctg	gcc	gcg	cag	ggc	ctg	tgg	gcg	cag	atg	tcc	gtg	ttc	cac	cga	1354
Leu	Leu	Ala	Ala	Gln	Gly	Leu	Trp	Ala	Gln	Met	Ser	Val	Phe	His	Arg	
				420				425					430			
gag	gac	ctg	gaa	agg	ctc	ggg	gtg	cag	gag	tcc	gac	ctc	cgt	ctg	ttc	1402
Glu	Asp	Leu	Glu	Arg	Leu	Gly	Val	Gln	Glu	Ser	Asp	Leu	Arg	Leu	Phe	
		435					440					445				

FIG. 17B

ctg gac gga gac atc ctc cgc cag gac aga gtc tcc aaa ggc tgc tac	1450
Leu Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr	
450 455 460	
tcc ttc atc cac ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac	1498
Ser Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr	
465 470 475 480	
gcc ctg gag aag gag gag ggg gag gac agg gac ggc cac gcc tgg gac	1546
Ala Leu Glu Lys Glu Glu Gly Glu Asp Arg Asp Gly His Ala Trp Asp	
485 490 495	
atc ggg gac gta cag aag ctg ctt tcc gga gaa gaa aga ctc aag aac	1594
Ile Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn	
500 505 510	
ccc gac ctg att caa gta gga cac ttc tta ttc ggc ctc gct aac gag	1642
Pro Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu	
515 520 525	
aag aga gcc aag gag ttg gag gcc act ttt ggc tgc cgg atg tca ccg	1690
Lys Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro	
530 535 540	
gac atc aaa cag gaa ttg ctg caa tgc aaa gca cat ctt cat gca aat	1738
Asp Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn	
545 550 555 560	
aag ccc tta tcc gtg acc gac ctg aag gag gtc ttg ggc tgc ctg tat	1786
Lys Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr	
565 570 575	
gag tct cag gag gag gag ctg gcg aag gtg gtg gtg gcc ccg ttc aag	1834
Glu Ser Gln Glu Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys	
580 585 590	
gaa att tct att cac ctg aca aat act tct gaa gtg atg cat tgt tcc	1882
Glu Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser	
595 600 605	
ttc agc ctg aag cat tgt caa gac ttg cag aaa ctc tca ctg cag gta	1930
Phe Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val	
610 615 620	
gca aag ggg gtg ttc ctg gag aat tac atg gat ttt gaa ctg gac att	1978
Ala Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile	
625 630 635 640	
gaa ttt gaa agg tgc act tac cta acc att ccg aac tgg gct cgg cag	2026
Glu Phe Glu Arg Cys Thr Tyr Leu Thr Ile Pro Asn Trp Ala Arg Gln	
645 650 655	
gat ctt cgc tct ctt cgc ctc tgg aca gat ttc tgc tct ctc ttc agc	2074
Asp Leu Arg Ser Leu Arg Leu Trp Thr Asp Phe Cys Ser Leu Phe Ser	
660 665 670	

FIG. 17C

tca aac agc aac ctc aag ttt ctg gaa gtg aaa caa agc ttc ctg agt 2122
 Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser Phe Leu Ser
 675 680 685

gac tct tct gtg cgg att ctt tgt gac cac gta acc cgt agc acc tgt 2170
 Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg Ser Thr Cys
 690 695 700

cat ctg cag aaa gtg gag att aaa aac gtc acc cct gac acc gcg tac 2218
 His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp Thr Ala Tyr
 705 710 715 720

cgg gac ttc tgt ctt gct ttc att ggg aag aag acc ctc acg cac ctg 2266
 Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu Thr His Leu
 725 730 735

acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg ctg atg ctg 2314
 Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met Leu Met Leu
 740 745 750

tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac ctg agg ttg 2362
 Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr Leu Arg Leu
 755 760 765

gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc ttc tat gtc 2410
 Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe Phe Tyr Val
 770 775 780

ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca gcc aat gtg 2458
 Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser Ala Asn Val
 785 790 795 800

ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg aca cgc cca 2506
 Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met Thr Arg Pro
 805 810 815

aaa cac ttc ctg cag atg ttg tgc ttg gaa aac tgt cgt ctt aca gaa 2554
 Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg Leu Thr Glu
 820 825 830

gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc aag aag ctg 2602
 Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser Lys Lys Leu
 835 840 845

aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca ggg gtg aag 2650
 Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr Gly Val Lys
 850 855 860

ttt ctg tgt gag ggc ttg agt tac cct gat tgt aaa ctg cag acc ttg 2698
 Phe Leu Cys Glu Gly Leu Ser Tyr Pro Asp Cys Lys Leu Gln Thr Leu
 865 870 875 880

gtg tta cag caa tgc agc ata acc aag ctt ggc tgt aga tat ctc tca 2746
 Val Leu Gln Gln Cys Ser Ile Thr Lys Leu Gly Cys Arg Tyr Leu Ser
 885 890 895

FIG. 17D



gag gcg ctc caa gaa gcc tgc agc ctc aca aac ctg gac ttg agt atc	2794
Glu Ala Leu Gln Glu Ala Cys Ser Leu Thr Asn Leu Asp Leu Ser Ile	
900 905 910	
aac cag ata gct cgt gga ttg tgg att ctc tgt cag gca tta gag aat	2842
Asn Gln Ile Ala Arg Gly Leu Trp Ile Leu Cys Gln Ala Leu Glu Asn	
915 920 925	
cca aac tgt aac cta aaa cac cta cgg ttg aag acc tat gaa act aat	2890
Pro Asn Cys Asn Leu Lys His Leu Arg Leu Lys Thr Tyr Glu Thr Asn	
930 935 940	
ttg gaa atc aag aag ctg ttg gag gaa gtg aaa gaa aag aat ccc aag	2938
Leu Glu Ile Lys Lys Leu Leu Glu Glu Val Lys Glu Lys Asn Pro Lys	
945 950 955 960	
ctg act att gat tgc aat gct tcc ggg gca acg gca cct ccg tgc tgt	2986
Leu Thr Ile Asp Cys Asn Ala Ser Gly Ala Thr Ala Pro Pro Cys Cys	
965 970 975	
gac ttt ttt tgc tgagcagcct gggatcgctc tacgaattac acaggaagcg	3038
Asp Phe Phe Cys	
980	
ggattcgggt ctctaagatg tcttatgaat gcagggtcaga gggtcacatg ttaacactag	3098
agtctgtcga gaggtaggat ttgacactgg ttttctcact atttttgga gattctgcac	3158
gagtcacgca ccccttcac atgacgctat gtactttctc acagggataa taaagttaga	3218
gcactctcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa	3263

FIG. 17E

48

atg gca gaa tcg gat tct act gac ttt gac ctg ctg tgg tat cta gag	48
Met Ala Glu Ser Asp Ser Thr Asp Phe Asp Leu Leu Trp Tyr Leu Glu	
1 5 10 15	
aat ctc agt gac aag gaa ttt cag agt ttt aag aag tat ctg gca cgc	96
Asn Leu Ser Asp Lys Glu Phe Gln Ser Phe Lys Lys Tyr Leu Ala Arg	
20 25 30	
aag att ctt gat ttc aaa ctg cca cag ttt cca ctg ata cag atg aca	144
Lys Ile Leu Asp Phe Lys Leu Pro Gln Phe Pro Leu Ile Gln Met Thr	
35 40 45	
aaa gaa gaa ctg gct aac gtg ttg cca atc tct tat gag gga cag tat	192
Lys Glu Glu Leu Ala Asn Val Leu Pro Ile Ser Tyr Glu Gly Gln Tyr	
50 55 60	
ata tgg aat atg ctc ttc agc ata ttt tca atg atg cgt aag gaa gat	240
Ile Trp Asn Met Leu Phe Ser Ile Phe Ser Met Met Arg Lys Glu Asp	
65 70 75 80	
ctt tgt agg aag atc att ggc aga cga aac cat gtg ttc tac ata ctt	288
Leu Cys Arg Lys Ile Ile Gly Arg Arg Asn His Val Phe Tyr Ile Leu	
85 90 95	
caa tta gcc tat gat tct acc agc tat tat tca gca aac aat ctc aat	336
Gln Leu Ala Tyr Asp Ser Thr Ser Tyr Tyr Ser Ala Asn Asn Leu Asn	
100 105 110	
gtg ttc ctg atg gga gag aga gca tct gga aaa act att gtt ata aat	384
Val Phe Leu Met Gly Glu Arg Ala Ser Gly Lys Thr Ile Val Ile Asn	
115 120 125	
ctg gct gtg ttg agg tgg atc aag ggt gag atg tgg cag aac atg atc	432
Leu Ala Val Leu Arg Trp Ile Lys Gly Glu Met Trp Gln Asn Met Ile	
130 135 140	
tcg tac gtc gtt cac ctc act tct cac gaa ata aac cag atg acc aac	480
Ser Tyr Val Val His Leu Thr Ser His Glu Ile Asn Gln Met Thr Asn	
145 150 155 160	
agc agc ttg gct gag cta atc gcc aag gac tgg cct gac ggc cag gct	528
Ser Ser Leu Ala Glu Leu Ile Ala Lys Asp Trp Pro Asp Gly Gln Ala	
165 170 175	
ccc att gca gac atc ctg tct gat ccc aag aaa ctc ctt ttc att ctc	576
Pro Ile Ala Asp Ile Leu Ser Asp Pro Lys Lys Leu Leu Phe Ile Leu	
180 185 190	
gag gac ttg gac aac ata aga ttc gag tta aat gtc aat gaa agt gct	624
Glu Asp Leu Asp Asn Ile Arg Phe Glu Leu Asn Val Asn Glu Ser Ala	
195 200 205	
ttg tgt agt aac agc acc cag aaa gtt ccc att cca gtt ctc ctg gtc	672
Leu Cys Ser Asn Ser Thr Gln Lys Val Pro Ile Pro Val Leu Leu Val	
210 215 220	

FIG. 18A

agt	ttg	ctg	aag	aga	aaa	atg	gct	cca	ggc	tgc	tgg	ttc	ctc	atc	tcc	
Ser	Leu	Leu	Lys	Arg	Lys	Met	Ala	Pro	Gly	Cys	Trp	Phe	Leu	Ile	Ser	
225					230					235					240	
tca	agg	ccc	aca	cgt	ggg	aat	aat	gta	aaa	acg	ttc	ttg	aaa	gag	gta	
Ser	Arg	Pro	Thr	Arg	Gly	Asn	Asn	Val	Lys	Thr	Phe	Leu	Lys	Glu	Val	
				245					250					255		
gat	tgc	tgc	acg	acc	ttg	cag	ctg	tgc	aat	ggg	aag	agg	gag	ata	tat	816
Asp	Cys	Cys	Thr	Thr	Leu	Gln	Leu	Ser	Asn	Gly	Lys	Arg	Glu	Ile	Tyr	
			260					265					270			
ttt	aac	tct	ttc	ttt	aaa	gac	cgc	cag	agg	gcg	tgc	gca	gcc	ctc	cag	864
Phe	Asn	Ser	Phe	Phe	Lys	Asp	Arg	Gln	Arg	Ala	Ser	Ala	Ala	Leu	Gln	
		275					280					285				
ctt	gta	cat	gag	gat	gaa	ata	ctc	gtg	ggc	ctg	tgc	cga	gtc	gcc	atc	912
Leu	Val	His	Glu	Asp	Glu	Ile	Leu	Val	Gly	Leu	Cys	Arg	Val	Ala	Ile	
	290					295					300					
tta	tgc	tgg	atc	acg	tgt	act	gtc	ctg	aag	cgg	cag	atg	gac	aag	ggg	960
Leu	Cys	Trp	Ile	Thr	Cys	Thr	Val	Leu	Lys	Arg	Gln	Met	Asp	Lys	Gly	
305					310					315					320	
cgt	gac	ttc	cag	ctc	tgc	tgc	caa	aca	ccc	act	gat	cta	cat	gcc	cac	1008
Arg	Asp	Phe	Gln	Leu	Cys	Cys	Gln	Thr	Pro	Thr	Asp	Leu	His	Ala	His	
				325					330					335		
ttt	ctt	gct	gat	gcg	ttg	aca	tca	gag	gct	gga	ctt	act	gcc	aat	cag	1056
Phe	Leu	Ala	Asp	Ala	Leu	Thr	Ser	Glu	Ala	Gly	Leu	Thr	Ala	Asn	Gln	
			340					345					350			
tat	cac	cta	ggc	ctc	cta	aaa	cgt	ctg	tgt	ttg	ctg	gct	gca	gga	gga	1104
Tyr	His	Leu	Gly	Leu	Leu	Lys	Arg	Leu	Cys	Leu	Leu	Ala	Ala	Gly	Gly	
		355					360					365				
ctg	ttt	ctg	agc	acc	ctg	aat	ttc	agt	ggc	gaa	gac	ctc	aga	tgt	gtt	1152
Leu	Phe	Leu	Ser	Thr	Leu	Asn	Phe	Ser	Gly	Glu	Asp	Leu	Arg	Cys	Val	
	370					375					380					
ggg	ttt	act	gag	gct	gat	gtc	tct	gtg	ttg	cag	gcc	gcg	aat	att	ctt	1200
Gly	Phe	Thr	Glu	Ala	Asp	Val	Ser	Val	Leu	Gln	Ala	Ala	Asn	Ile	Leu	
385					390					395					400	
ttg	ccg	agc	aac	act	cat	aaa	gac	cgt	tac	aag	ttc	ata	cac	ttg	aac	1248
Leu	Pro	Ser	Asn	Thr	His	Lys	Asp	Arg	Tyr	Lys	Phe	Ile	His	Leu	Asn	
				405					410					415		
gtc	cag	gag	ttt	tgt	aca	gcc	att	gca	ttt	ctg	atg	gca	gta	ccc	aac	1296
Val	Gln	Glu	Phe	Cys	Thr	Ala	Ile	Ala	Phe	Leu	Met	Ala	Val	Pro	Asn	
			420					425					430			
tat	ctg	atc	ccc	tca	ggc	agc	aga	gag	tat	aaa	gag	aag	aga	gaa	caa	1344
Tyr	Leu	Ile	Pro	Ser	Gly	Ser	Arg	Glu	Tyr	Lys	Glu	Lys	Arg	Glu	Gln	
		435					440					445				

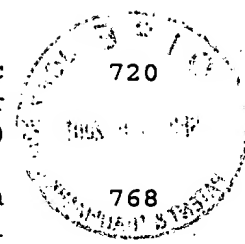


FIG. 18B

tac tct gac ttt aat caa gtg ttt act ttc att ttt ggt ctt cta aat Tyr Ser Asp Phe Asn Gln Val Phe Thr Phe Ile Phe Gly Leu Leu Asn 450 455 460	1392
gca aac agg aga aag att ctt gag aca tcc ttt gga tac cag cta ccg Ala Asn Arg Arg Lys Ile Leu Glu Thr Ser Phe Gly Tyr Gln Leu Pro 465 470 475 480	1440
atg gta gac agc ttc aag tgg tac tcg gtg gga tac atg aaa cat ttg Met Val Asp Ser Phe Lys Trp Tyr Ser Val Gly Tyr Met Lys His Leu 485 490 495	1488
gac cgt gac ccg gaa aag ttg acg cac cat atg cct ttg ttt tac tgt Asp Arg Asp Pro Glu Lys Leu Thr His His Met Pro Leu Phe Tyr Cys 500 505 510	1536
ctc tat gag aat cgg gaa gaa gaa ttt gtg aag acg att gtg gat gct Leu Tyr Glu Asn Arg Glu Glu Glu Phe Val Lys Thr Ile Val Asp Ala 515 520 525	1584
ctc atg gag gtt aca gtt tac ctt caa tca gac aag gat atg atg gtc Leu Met Glu Val Thr Val Tyr Leu Gln Ser Asp Lys Asp Met Met Val 530 535 540	1632
tca tta tac tgt ctg gat tac tgc tgt cac ctg agg aca ctt aag ttg Ser Leu Tyr Cys Leu Asp Tyr Cys Cys His Leu Arg Thr Leu Lys Leu 545 550 555 560	1680
agt gtt cag cgc atc ttt caa aac aaa gag cca ctt ata agg cca act Ser Val Gln Arg Ile Phe Gln Asn Lys Glu Pro Leu Ile Arg Pro Thr 565 570 575	1728
gct agt caa atg aag agc ctt gtc tac tgg aga gag atc tgc tct ctt Ala Ser Gln Met Lys Ser Leu Val Tyr Trp Arg Glu Ile Cys Ser Leu 580 585 590	1776
ttt tat aca atg gag agc ctc cgg gag ctg cat atc ttt gac aat gac Phe Tyr Thr Met Glu Ser Leu Arg Glu Leu His Ile Phe Asp Asn Asp 595 600 605	1824
ctt aat ggt att tca gaa agg att ctg tct aaa gcc ctg gag cat tct Leu Asn Gly Ile Ser Glu Arg Ile Leu Ser Lys Ala Leu Glu His Ser 610 615 620	1872
agc tgt aaa ctt cgc aca ctc aag ttg tcc tat gtc tcg act gct tct Ser Cys Lys Leu Arg Thr Leu Lys Leu Ser Tyr Val Ser Thr Ala Ser 625 630 635 640	1920
ggg ttt gaa gac tta ctc aag gct ttg gct cgt aat cgg agc ctg aca Gly Phe Glu Asp Leu Leu Lys Ala Leu Ala Arg Asn Arg Ser Leu Thr 645 650 655	1968
tac ctg agt atc aac tgt acg tcc att tcc cta aat atg ttt tca ctt Tyr Leu Ser Ile Asn Cys Thr Ser Ile Ser Leu Asn Met Phe Ser Leu 660 665 670	2016

FIG. 18C

ctg cat gac atc ctg cac gag ccc aca tgc caa ata agt cat ctg agc 2064
 Leu His Asp Ile Leu His Glu Pro Thr Cys Gln Ile Ser His Leu Ser
 675 680 685

ttg atg aaa tgt gat ttg cga gcc agc gaa tgc gaa gaa atc gcc tct 2112
 Leu Met Lys Cys Asp Leu Arg Ala Ser Glu Cys Glu Glu Ile Ala Ser
 690 695 700

ctc ctc atc agt ggc ggg agt ctg aga aaa ctg acc tta tcc agc aat 2160
 Leu Leu Ile Ser Gly Gly Ser Leu Arg Lys Leu Thr Leu Ser Ser Asn
 705 710 715 720

ccg ctg agg agc gac ggg atg aac ata ctg tgt gat gcc ttg ctt cat 2208
 Pro Leu Arg Ser Asp Gly Met Asn Ile Leu Cys Asp Ala Leu Leu His
 725 730 735

ccc aac tgc act ctt ata tca ctg gtt ctg tct ggc tgt ttc ttt agc 2256
 Pro Asn Cys Thr Leu Ile Ser Leu Val Leu Ser Gly Cys Phe Phe Ser
 740 745 750

agc gat atc tgt caa tat att gcc ata gtt att gct act aat gaa aaa 2304
 Ser Asp Ile Cys Gln Tyr Ile Ala Ile Val Ile Ala Thr Asn Glu Lys
 755 760 765

ctg agg agc ctg gag att ggg agc aac aaa ata gaa gat gca gga atg 2352
 Leu Arg Ser Leu Glu Ile Gly Ser Asn Lys Ile Glu Asp Ala Gly Met
 770 775 780

cag ctg cta tgt ggt ggt ttg aga cat ccc aac tgc atg ttg gtg aat 2400
 Gln Leu Leu Cys Gly Gly Leu Arg His Pro Asn Cys Met Leu Val Asn
 785 790 795 800

att ggg cta gaa gag tgc atg tta acc agt gcc tgc tgt cga tct ctt 2448
 Ile Gly Leu Glu Glu Cys Met Leu Thr Ser Ala Cys Cys Arg Ser Leu
 805 810 815

gcc tct gtt ctt acc acc aac aaa aca cta gaa aga ctc aac ttg ctt 2496
 Ala Ser Val Leu Thr Thr Asn Lys Thr Leu Glu Arg Leu Asn Leu Leu
 820 825 830

caa aat cac ttg ggc aat gat gga gtt gca aaa ctt ctt gag agc ttg 2544
 Gln Asn His Leu Gly Asn Asp Gly Val Ala Lys Leu Leu Glu Ser Leu
 835 840 845

atc agc cca gat tgt gta ctt aag gta gtt ggc ttg atg gct gct gag 2592
 Ile Ser Pro Asp Cys Val Leu Lys Val Val Gly Leu Met Ala Ala Glu
 850 855 860

aac atg gag tcc ctc att ccc agg cca gca cgc tga 2628
 Asn Met Glu Ser Leu Ile Pro Arg Pro Ala Arg
 865 870 875

FIG. 18D